

1 GAATTGGCC CTCGAGGCC AGAATTGGC ACGAGGGCG GCGCCAGGC CAGGCAGAGC GCTGTCGAT CCCGGCGTC CACCCGCCAT GGGGCTCTCC
 CTTAACCGG GAGCTCCGGT TCTTAAGCCG TGCTCCGGC CGCGGGGTGCG GTCCGCTCTCG CGACAGCGTA GGGCCCGCAG GTGGGGCGGTA CCCCAGAGG
 1 Me tGlyLeuSer

101 TGGAGCCCG GACCTCCACT GCTGATGATC CTGCTACTGG TGCTGTCGTT GTGGCTGCCA CTGGAGGAG GAAACTCCCT TGCCACAGAG AACAGGTTTG
 ACCTCGGGCG CTGGAGGTGA CGACTACTAG GACGATGACC ACGACAGCAA CACCGACGGT GAAACAGGGT CTTGAGGGAA ACCGCTCGTC TTGTCACAAAC
 5 TrpSerProA rgProProLe uLeuMetIle LeuLeuLeuV alleuSerLe utRpleuPro LeuGlyAlaG lyAsnSerLe uAlaThrGlu AsnArgPheVal

201 TGAACAGGCTG TACCCAGGCC AGAAAAGAAAT GCGAGGCTAA TCCCGCTGTC AAGGCTGGCT ACCAGGACTT GGGCTCCCTGC ACCCTCCAGTT TAAGGAGGCC
 AcTGTGAC ATCGGTCCGG TCTTCTTTA CGCTCCGATT AGGGCGAACG TTCCGACCGGA TGGTCGTGGA CCCGAGGACG TGGAGGTCAA ATTGTCCTGG
 39 AsnSerCysThrGlnAla ArgLysLysCys ysgluAlaAs nProAlaCys LysAlaAlaT yrGlnHisLe uGlySerCys ThrSerSerL euSerArgPro

301 GCTGCCCTTA GAGGAGTCTG CCATGTCG AGACTGCTCA GAGGCCAGG AACAACTCAG GAACAGCTCT GAACAGCTCT CTGATAGACT GCAGGTGCCA TCGGGCATG
 CGACCGGAAT CTCCTCAGAC GGTACAGAC TCTGACGGAT CTCCGCTGTC TTGTCGAGTC CTTGTCGAGA GACTATCTGA GTTGCACGGT AGCCGGTAC
 72 LeuProLeu GluGluUserA 1aMetSer1 aAspCysLeu GluAlaAlaG lugInLeuAaR gAsnSerSer LeuIleAspC yArgCysHi sArgGmet

401 AAGCACCAAG CTACCTGTCT GGACATTAT TGGACCGTTT ACCCAGCTGGT AAGCCTGGT GACTACGAGT TGGATGTC ACCCTATGAA GACACAGTGA
 TTGCTGGTTC GATGGACAGA CCTGTAATA ACCTGGCAAG TGGGACGGG TTGGAACCA CTGATGCTCA ACCTACAGAG TGGGATACTT CTGTCAC
 105 LysHisGlnA lathrCysLe wAspIleTyR TrpThrValH isProAlaAar gSerLeuGly AspTyrgluL euAspValSe rProTyrglu AspThrValThr

501 CCGGAAACC CTGGAAAATG AATCTTAGCA AGTGTAACT GCTGAAACCA GACTGGGACC TCTGCCCTAA ATTGCTATG CTGTTACTC TTCACGACAA
 GGTCTGTTGG GACTTTTAC TTGAAATCTGT TCAACTTGTGTA CGAGTTGGT CTGAGCCTGG AGACGGAGTT TAAACGATAC GACACATGAG AAGTGTGTT
 139 SerLysPr oTrpLysMet AsnLeuSerL yLeuAsnMe tLeuLysPro AspSerAspL euCysLeuL sPheAlaMet LeuCysThrL euHisAspLys

601 GTGTGACCGC CTGGCAAGG CCTACGGGA GGCATGCTCA GGGATCCGCTT GCCAGGCCA CCTCTGCTTA GCCCAGCTGC GCTCCTCTT TGAGAAGCA
 CACACTGGCG GACGGTTC GGATGCCCT CGGTACGAGT CCCTAGGGGA CGGTGCGGGT GGAGACGGAT CGGGTCGAGC CGAGGAAGAA ACTCTCCGT
 172 CysAspArg LeuArgLysA 1aTyrGlyG1 uAlaCysSer GlyTleArgC ysglnArgHi sLeuCysLeu AlaGlnLeuA rgSerPhePh eGluLysAla

701 GCAGAGTCCC ACGCTCAGGG TCTGCTGCTG TGTCCTGTG CACCAAGAGA TGGGGCTGT GGGGAGGGC GGCCTAACAC CATGGCCCCC AGTTGGCCC
 CGTCTCAGGG TGGAGTCCC AGACGAGAC ACAGGGACAC GTGGTCTCT ACGGGACAC CCCCTCGCG CGCGATTGTG GTAGGGGGG TCAACGGGG
 205 AlaGluUserH isAlaGlnG1 yLeuLeuLeu CysProCysA 1aProGluAspA palAgluLysA GlyGluArgA rgArgAsnHt rIleAlaPro SerCysAlaLeu

801 TGCCTTCTGT AACCCCCAAT TGCCTGGATC TGCGGAGCTT CTGGCGTGG CACCTTTGT GCAGATCAG CCTGATGGAC TTCCAGACCC ACTGTCATCC
 ACGGAAAGACA TTGGGGTTA ACGGACCTAG ACGGCTCGAA GACGGCACG GACGGCACGC CTGGAAACA CGTCTAGTGC GGACTACCTG AAGGCTCTGG TGACAGTAGG
 239 ProSerVa 1IthrProAsn CysLeuAspL euArgSerPh eCysArgAla AspProLeuC yAspSerCysA gLeuMetAsp PheGlnThrH isCysHi Pro

901 TATGGACATC CTTGGGACTT GTGCAACTGA GCAGTCCAGA TGTCTGGGG CATACTGGG GCTGATTGGG ACTGCTCATGA CCCAAACTT CATCAGCAAG
 ATACCTGTAG GAACCCCTGA CACCTTGACT CGTCAGGTCT ACAGACGGCC GTATGGACCC CGACTAAACCC TGACGGTACT GGGGTTGAA GTAGTCGTT
 272 MetAspIle LeuGlyThrC ysglnSerArg CysLeuArgA 1aTyrLeuG1 yLeuIleGly ThrAlaMetT hrProAsnPh elleSerLys

FIG. 1A

1001 GTCAACACTA CTGTTGCCCT AAGCTGCACC TGCCGAGGCA GGGCAACCT ACAGGACGAG TGTGAACAGC TGGAAAGGTC CTTCTCCAG AACCCCTGCC
 CAGTGTGAT GACAACGAA TTGAGCTGG ACGGCTCCGT CGCCGTTGGA TGTCTGCTC ACACCTGTG ACCTTTCAG GAAGGGGTC TTGGGACGG
 305 ValAsnThr hrValAlaLe uSerCysThr CysArgGlyS erglyAsnLe uGlnAspGlu CysGluGlnL eugluArgSe rPheSerGln AsnProCysLeu

1101 TCGTGAGGG CATTGAGGT AAGATGGTT TCCACAGACA GCTCTTCCTCC CAGGACTGGG CAGACTCTAC TTTTTCACTG GTGAGGAGC AGAACAGCAA
 AGCACCTCCG GTAACGTCGA TTCTACGAA AGGTGTCGTG CGAGAAAGGG GTCTGACCC GTCTGAGATG AAAAAGTCAC CACGTCGTG TCTTGTGTT
 339 ValGluAl aileAlaAla LysMetArgP heHisArgP nLeuPheSer GlnAspPtpA 1aAspSerVal rPheSerVal ValGlnGlnG lnAsnSerAsn

1201 CCCTGCTCTG AGACTGAGCC CCAGGCTTAC CAJTCCTTCT TTCTCCATCC TTGCTGTGAG ACCCCTCTGGT AGCTGGGCTT CCTCAAGGGT
 GGGACGAGAC TCTGACGTCG GGTCCGATGG GTAAAGAAAAGA AAGAGGTAGG AAGGAAACTA AGACGACGTC TGGAGACCA TCAGCCGAA GGAGTCCAG
 372 ProAlaLeu ArgLeuGlnP roArgLeuPr orileLeuSer PheSerIleL euProLeuI1 eLeuLeuGln ThrLeuTrp

1301 CTTTGCTCTC TCACCAACAC CCAGACTGAT TTGAGCTGGCTG TGGTGGGAGA GAACTCGCCA GCTGTGGAA GAAGAGCCAG CGTGTACAC AGCAACCCGG
 GAAACAGGG AGGTGGTGTG GGTCTGACTA AACGTCGGAC ACCACCTCTT CTTGAGCGGT CGGACACCTT CTTCGTCGTC GCACGATG TG TGTTGGGCC

1401 AACCAAACCG GCATTCGGCA GCACATCCCG TCTGCTCCAG AAGAGGTCTT AGAAGTGGGG GCTGTGACCC TTCCGATCCT GAGGGCTAG TTTTCAAACC
 TTGGCTTGTC CGTAAGGGGT CGTGTAGGGC AGACGAGGTG TTCTCCAGAA TCTTCAGTC CGACACTGGG AAGGCTAGGA CTCGCCGATC AAAAGTTGG

1501 TCCCTTGGCC CTGCTTCCTT CTGCTCCTCC TTAGGACTTT GTGGTCCAG TTTTGCTCTC TTGTTCTGATG GTGATTAGCG GCTCACCTCC
 AGGGAAACGGG GACGAAGGA GACCGAGTCC GACGGAGGG AAATCCGAA CACCCAGGT AAAACGGAG ACAAGACTAC CACTAATGCG CGAGTGGAGG

1601 AGCGCTCTCTT CCTGTTTCCC AGGACCAACCC AGAGGCTAAG GAATCAGTCA TTCCCTGTT CTTCTTCAG GAAGGGAGGC TAAGGGTCT GAGGTGACTG
 TCGCGAAAGAA GGACAAAGGG TCCTGGGG TCTCCGATC CTTAGTCAGT AAGGACAAC GGAAGGGTC CTTCGTCG ATTCCCAAGA CTCCACTGAC

1701 AGAAAATGT TTCTTGTG TGGAAGGCTG GTGCTCCAGC CTCCACGTC CTCGAATGG AAGATAAAA CCTGCTGGTG TCTGCACTGC AGAACGACAC
 TCTTTTACA AAGGAAACAC ACCTTCGAC CACGGAGTCG GAGGTGGAGG GAGACTTAC TTCTATTTC GGACTTAC AGAAACTGAGC AGACGGTCCG

1801 AATCCCTGAAC ATTGGGGCAT GAAGAGCTAA AGTCTTTGGG TCTTGTGTTAA CTCTCTATTAC TGTCCTATTAC TTCCCTCTAGT CCCTTGGGTC ATGATTAAC
 TTAGGGACTTG TAAACCCGTA CTTCCTGAA CTTCTGAA AGAACAAATT GAGGATAATG ACAGGGGTTT AAGGGATCA GGGAAACCCAG TACTAATTG

1901 ATTTTGACTT AAAAAAAAAA AAAAAA AAAAAA
 TAAACCTGAA TTTTTTTTTT TTTTTTTTTT TTTTT

FIG. 1B

rGFR α 1	1	WIFLATTLYFALPLLDLIMSAEVSSGG	•	DRLDCVKASDQCLKEQSCSSTK ^Y RT
rGFR α 2	1	MILANAFCLFFFIDETT ^{RS} LASR	•	SSLQGSELEHGWRPQVDCV ^Y RA
mGFR α 3	1	MGLSWSPRPPPLMILVLISWLPLG ^{AG} NSLATE	•	NELCAES ^{SS} SS ^Y RT
rGFR α 1	49	[RQC]VAGKET	•	[KQKS]LYNCACKRGMKKEKNC
rGFR α 2	60	[RQC]LAGRD	•	[RQC]VDCRCKRGMKKELOCLQIYWSI
mGFR α 3	61	[GSC]TSSLSPRLP	•	[RQC]VDCRACHARMKHOATCLDIYWTVHP
rGFR α 1	109	S[Q]GNDLLEDSPYEPVNSTR	•	[KQKS]LYNCACKRGMKKEKNC
rGFR α 2	115	G[TE]GEEFYEARSPYEPVT	•	[RQC]VDCRCKRGMKKELOCLQIYWSI
mGFR α 3	120	ARSLGDYEDDVSPYED	•	[RQC]VDCRACHARMKHOATCLDIYWTVHP
rGFR α 1	168	KKYRSAYTPCTTSM	•	[KQKS]LYNCACKRGMKKEKNC
rGFR α 2	175	KKLASSYISICNREISPT	•	[RQC]VDCRCKRGMKKELOCLQIYWSI
mGFR α 3	173	DRLRKA[Y]GEAC	•	[RQC]VDCRACHARMKHOATCLDIYWTVHP
rGFR α 1	225	RRQTVPVCSYEEER	•	[KQKS]LYNCACKRGMKKEKNC
rGFR α 2	233	RRQTLPSCSYEDKEK	•	[RQC]VDCRCKRGMKKELOCLQIYWSI
mGFR α 3	228	RRNTIAPSC	•	[RQC]VDCRACHARMKHOATCLDIYWTVHP
rGFR α 1	285	CLAYSGLTGTVMT	•	[KQKS]LYNCACKRGMKKEKNC
rGFR α 2	293	CLGSYAGM	•	[RQC]VDCRCKRGMKKELOCLQIYWSI
mGFR α 3	285	CLRAYLGI	•	[RQC]VDCRACHARMKHOATCLDIYWTVHP
rGFR α 1	343	QAFGNGSSEVT	•	[KQKS]LYNCACKRGMKKEKNC
rGFR α 2	353	QAFGNGSSEVNM	•	[RQC]VDCRCKRGMKKELOCLQIYWSI
mGFR α 3	343	AA	•	[RQC]VDCRACHARMKHOATCLDIYWTVHP
rGFR α 1	403	KSNSG	•	[KQKS]LYNCACKRGMKKEKNC
rGFR α 2	410	LSMCFT	•	[RQC]VDCRCKRGMKKELOCLQIYWSI
mGFR α 3	345	ELSMCFT	•	[RQC]VDCRACHARMKHOATCLDIYWTVHP
rGFR α 1	463	S[LAETS	•	[KQKS]LYNCACKRGMKKEKNC
mGFR α 3	392	LLQTLW	•	[RQC]VDCRCKRGMKKELOCLQIYWSI

FIG. 2

hGFRa3	1	M V R P [L N P R P] L P P V V L M [L L L] L P P S P P L P L A A G D P L P T E S R L M N S C L Q A R R K
mGFRa3	1	- M G L S W S P P R P P L M I L L V L S L W . L P L G A G N S L A T E N R F V N S C T Q A R K K
hGFRa3	51	C Q A D P T C S A Y H H L D S C T S S I S T P L P S E E P S V P A D C L E A A Q Q L R N S S L I G
mGFRa3	48	C E A N P A C K A Y Q H L G S C T S S L S R P L P L E E S A M S A D C L E A E Q L R N S S L I D
hGFRa3	101	C M C H A R M K N Q V A C L D I Y W T V H P A R S L G N Y E L D V S P P Y E D T V T S K P W K M N L S
mGFRa3	98	C R C H A R M K H Q A T C L D I Y W T V H P A R S L G D Y E L D V S P P Y E D T V T S K P W K M N L S
hGFRa3	151	K L N M L K P D S D L C L K F A M L C T L N D K C D R L R K A Y G E A C S G P H C Q R H V C L R Q L
mGFRa3	148	K L N M L K P D S D L C L K F A M L C T L H D K C D R L R K A Y G E A C S G I R C Q R H L C L A Q L
hGFRa3	201	L T F F E K A A E P H A Q G L L L C P C A P N D R G C G E R R R N T I A P N C A L P P V A P N C L E
mGFRa3	198	R S F F E K A A E S H A Q G L L L C P C A P E D A G C G E R R R N T I A P S C A L P S V T P N C L D
hGFRa3	251	L R R L C F S D P L C R S R L V D F Q T H C H P M D I L G T C A T E Q S R C L R A Y L G L I G T A M
mGFRa3	248	L R S F C R A D P L C R S R L M D F Q T H C H P M D I L G T C A T E Q S R C L R A Y L G L I G T A M
hGFRa3	301	T P N F V S N V N T S V A L S C T C R G S G N L Q E E C M L E G F F S H N P C L T E A I A A K M R
mGFRa3	298	T P N F I S K V N T T V A L S C T C R G S G N L Q D E C E Q L E R S F S Q N P C L V E A I A A K M R
hGFRa3	351	F H S Q L F S Q D W P H P T F A V M A H Q N E N P A V R P Q P W V P S L F S C T L P L I L L S L W
mGFRa3	348	F H R Q L F S Q D W A D S T F S V V Q Q Q N S N P A L R L Q P R L P I L S F S I L P L I L L Q T L W

FIG. 3

FIG. 4

48613	1	M V R P L N P R P L P P V V L M L L L L P P S P L P L A A G D P L P T E S R L M N S C L Q A R K
48614	1	M V R P L N P R P L P P V V L M L L L L P P S P L P L A A G D P L P T E S R L M N S C L Q A R K
48613	51	C Q A D P T C S A A Y H H L D S C T S I S T P L P S E E P S V P A D C L E A A Q Q L R N S S L I G
48614	51	C Q A D P T C S A A Y H H L D S C T S I S T P L P S E E P S V P A D C L E A A Q Q L R N S S L I G
48613	101	C M C H R R M K N Q V A C L D I Y W T V H R A R S L G N Y E L D V S P Y E D T V T S K P W K M N L S
48614	101	C M C H R R M K N Q V A C L D I Y W T V H R A R S L .
48613	151	K L N M L K P D S D L C L K F A M L C T L N D K C D R L R K A Y G E A C S G P H C Q R H V C L R Q L
48614	127 D S D L C L K F A M L C T L N D K C D R L R K A Y G E A C S G P H C Q R H V C L R Q L
48613	201	L T F F E K A A E P H A Q G L L C P C A P N D R G C G E R R A N T I A P N C A L P P V A P N C E
48614	170	L T F F E K A A E P H A Q G L L C P C A P N D R G C G E R R A N T I A P N C A L P P V A P N C E
48613	251	L R R L C F S D P L C R S R L V D F Q T H C H P M D I L G T C A T E Q S R C L R A Y L G L I G T A M
48614	220	L R R L C F S D P L C R S R L V D F Q T H C H P M D I L G T C A T E Q S R C L R A Y L G L I G T A M
48613	301	T P N F V S N V N T S V A L S C T C R G S G N L Q E E C E M L E G F F S H N P C L T E A I A A K M R
48614	270	T P N F V S N V N T S V A L S C T C R G S G N L Q E E C E M L E G F F S H N P C L T E A I A A K M R
48613	351	F H S Q L F S Q D W P H P T F A V M A H Q N E N P A V R P Q P W V P S L F S C T L P L I L L S I W
48614	320	F H S Q L F S Q D W P H P T F A V M A H Q N E N P A V R P Q P W V P S L F S C T L P L I L L S I W

DNA48613.orf	1	ATGGTGC	CCCCCTGAAC	CCGGAA	CCCC	TGCC	TAGTC	CGATGTT					
GDNFra1.orf	1	ATGTT					
GDNFra2.orf	1	ATGAT	CTTG	GC	AAACG	TCTTC	TCTCT	TCTTCT	TCTTCT	
DNA48613.orf	51	GCTGCT	GGCTGCC	GCGT	GGCC	GCTCG	GGCC	GCTCT	GGCC	GCTCT	GGCC	GACCCC	GACCCC
GDNFra1.orf	6	CCTGGC	GACCC	CTG	CTT	GGCTG	CTT	GGCTG	CTT	GGCTG	CTT	GGCTG	CTT
GDNFra2.orf	39	AGACGG	AGACCC	TCCG	GCTC	TGGC	CA	GCCC	CT	CCC	CT	GGCC	CT
DNA48613.orf	101	TTCC	CCACAGAA	GGCCGAC	TCA	TGAA	CAAGC	CTGTC	CCAG	GGCC	AGGAA	GAGGAA	GAGGAA
GDNFra1.orf	56	CCGAAGT	GAGCCG	GCGGAG	ACCC	GCCCT	TGGAA	TTGCG	TGAA	AGGAA	GGCAAGT	GATCAG	GATCAG
GDNFra2.orf	89	AGCT	CA	GGCTGG	CC	CC	CA	GTGG	GTCC	GGCC	GGCC	GGCC	GGCC
DNA48613.orf	151	TG	GCATGGCT	TGATCCC	CC	CTGCA	GAGT	GCTG	CCTAC	ACAC	CTGG	ATTC	GGATTCC
GDNFra1.orf	106	TG	GCCTGA	GAAGG	GG	AGGCA	AGGCT	GGCA	AGTAC	CCGG	CA	GGCA	AGT
GDNFra2.orf	139	TG	TGCC	GGCG	GA	ATCCAA	ACTGGC	CTCG	GCTAC	CCGG	CA	GGCA	AGT
DNA48613.orf	201	CA	CCTCTAG	CCATAG	GCAC	CC	CACTG	GGCT	CC	CTG	GGCT	TCGG	TCGG
GDNFra1.orf	156	CGT	GGGG	GGCA	AGG	GAG	CCAACT	TCA	GCCT	GGCA	ATGGCC	CTGG	AGGCCA
GDNFra2.orf	189	CCT	GGCA	GGG	CC	GG	CCAA	CCATGC	GC	CC	CTGG	CTGG	AGGCCA
DNA48613.orf	248	CT	GCTGACT	GGCTGG	CC	GGCA	AGCA	ACTC	AGGAA	ACAG	GGCT	CTGATA	CTGATA
GDNFra1.orf	206	AGG	ATGAG	GTGCC	GGCA	GG	CC	AT	TGAGG	CCTGAA	AGT	GGCT	CTAC
GDNFra2.orf	224	AC	AAGG	ATGCC	GG	CC	CC	TT	GGAGGT	CTTGAA	GGCC	GGCT	GTAC
DNA48613.orf	298	GG	CTGCA	TGT	GGCA	AC	CCGG	ATGAA	GGCA	GGCT	GGCT	GGACAT	GGACAT
GDNFra1.orf	256	AAC	TGGCC	GCTG	GGCA	AG	GGGG	GT	GAAGG	GAAGA	ACTG	GGCT	GGGCA
GDNFra2.orf	274	GAC	TGCC	GCTG	GGCA	AG	GGGG	CA	GAAGA	GGG	GCT	GGCA	GAT
DNA48613.orf	348	CT	ATT	TGGAC	CCGG	GT	GGCA	ATGAA	GGCA	GGCT	GGCT	GGACAT	GGACAT
GDNFra1.orf	306	TTA	CTGGG	GGCA	ATG	GT	GGCA	AGGAA	ATGAA	GGG	AGGAA	GGG	GGG
GDNFra2.orf	324	CTA	CTGGG	GGCA	AT	GGCA	GGGG	GT	GGCA	GGGG	GT	GGCA	GGGG

FIG. 5A

DNA48613.orf	398	TCTCCCCCTATGAAAG-	ACACAGTGACCCAGC
GDNFR1.orf	356	CCCATATGAAACCAAGTTA-	ACAGCAGATTTGTCA
GDNFR2.orf	374	CTCCCCCTATGAGCCGGGTGACCCCTCTCGGACATCTTCAGGCTT	CTTCAAGGCTT
DNA48613.orf	427	AACCCCTGGAAAATGAATCTCAGCA	ACTGAACATGCTCAACCAGACTC
GDNFR1.orf	388	GATATTCGGGTGGTCCATTCA	ATCAGTGGACACATTCCAAAGG
GDNFR2.orf	424	GCTCAATCTTCAGGACAGGGCA	GGTCAAGGCAAGAGAG
DNA48613.orf	477	AGACCTTGCCTCAAGTTGCATGGCTGTGTA	ACTCTCAATGACAAAGTGTG
GDNFR1.orf	438	GAACAACTGCCCAGGATGCA	ATCAGGCTGGAAACCTCGACATTGCA
GDNFR2.orf	474	CAACCATTTGCCCTGGATGCTGC	AGACCCGGAAACCTGAATGACAAC
DNA48613.orf	527	ACCGGCTGGCCAAAGGCCCTACGGGGAGGC	GGCCCGCACA
GDNFR1.orf	488	GAAGTACAGGGTCAAGGGGTACATCA	CCGGTGGCACCCAGCGT
GDNFR2.orf	524	GAAGGCTGGCTTCTACATCTCCAAAC	ATCTGCAAACCGGGAGATCTGGCA
DNA48613.orf	574	CAGCGCCACGGTCTGCCCTAGGCCAGCTGCT	ACTTTCTTCA
GDNFR1.orf	535	ATGATGCTGCAACCGCCAAAGTGC	CCAAAGGGCCCTCCGGCA
GDNFR2.orf	574	ACCGGAGGGCTGCAACCGGGCAAGTGC	CTACATCTGGCAAGTCTT
DNA48613.orf	624	CAGACGGCCATGCTACTGCCCCATGTGCCCA	GTGCCCA
GDNFR1.orf	585	TGACAAAGGTCCGGCCAAAGCAGCTACGG	GAATGCTCTTCTGGCTCC
GDNFR2.orf	624	CGACCGTGGCCAGCGAGTACACCTACGG	GGCATGCTCTTCTGGCTCC
DNA48613.orf	668	ACGACCGGGCTGGGGCCGGCAACACCATCGCCCCA	ACTGCCA
GDNFR1.orf	635	GGGACATCGCCCTGGCTGCTGCTGCTG	GGCTCTGCTGCTGCTGCTG
GDNFR2.orf	674	AAGACCAAGGGCGTGGGCTTGGCTTCTGGCTCC	GCTGCCAGCTGCCAG

5B
FIG

DNA48613.orf	718	G C C T G C C - - - G C C T G T G C C C C C C A A C T G C C T G G A G C T G C C C T C T G
GENFR1.orf	685	T C C T A T G A A G A G G G A A G C C C A A C T G T T T G A A T T T G C A G G A C T T C C T G
GENFR2.orf	724	T C C T A T G A G A C A A G G A A G C C C A A C T G C C T G G A C C T G G T G G T G G T G G
DNA48613.orf	765	C T T C T C C G A C C C G C T T T G C A G A T C A C G C C T G G A T T T C C A G C C A C T
GENFR1.orf	735	C A A G A C G A A T T A C A T C T G C A G A T C T C G C C T T G C G G A T T T T A C C A A C T
GENFR2.orf	774	C C G A C T G A C C A C C T G T C G G T C C C G G C T G G C A C T T C C A T G C C A A T T
DNA48613.orf	815	G C C A T C C C A T G G A C A T C C T A G G A A C T T G T G C A A C A G A G C A G T C C A G A - -
GENFR1.orf	785	G C C A G C C A G T C A A G G T C A G G C T A G C A G C T G C A G C A G C T G C C C T G C G G A C A T T A C C A G
GENFR2.orf	824	G T C G A G C C T C C T A C C A G A C G G T C A C C A G C C T G C G G A C A T T A C C A G
DNA48613.orf	862	- - - T G T C T A C G A G C A T A C C T G G G C T G A T T G G A C T G C C A T G A C C C C C A A
GENFR1.orf	835	G A C T G C T C C T C G C C T A C T C G G G C T T A T T G G C A G T C A G T G C A C C T
GENFR2.orf	874	G C G T G T C T G G G C T T A T G C T G G C A T G A T T G G T T G A C A T G A C A C C T T A A
DNA48613.orf	909	C T T T G T C A G C C A A T G T C A - - - - - A C A C C A G T G T G C C T T A A G C T G C A C C T
GENFR1.orf	885	C T A C A T A G A C T C C A G T A - - - - - G C C T C A G T G T G C C C C A T G G T G T G A C T
GENFR2.orf	924	C T A T G T G G A C T C C A G C C C C A C T G G C A T C G T G T G C C C C C T G G T G C A G G C T
DNA48613.orf	953	G C C G A G G C A G T G G C A A C C T G C A G G A G G A T G T G A A A T G C T G G A A G G G T T C
GENFR1.orf	929	G C A G C A A C A G T G G G A A C C G A C C T A G A A G A G T G C T G C C T T G A A A T T C T G A T T T C
GENFR2.orf	974	G T C G T G G C A G C G G G A A C A T G A G G A G G A T G T G A G A A G T T C C T C A G G G A C
DNA48613.orf	1003	T T C T C C C C A A C C C C T G C C T C A C G G A G G C C A T T G C A G G C C T A A G A T G C C G T T T
GENFR1.orf	979	T T C A A G G A C A A T A C A T G T C T T A A A A T G C A A T T C A A G G C C T T G G C A A T G G G
GENFR2.orf	1024	T T C A C C G A G A A C C C A T G C C T C C G G A A C G C C A T T C C A G G C C T T G G C A A C G G G

FIG. 5C

FIG. 5D

	DNA48613	GDNFRa1	GDNFRa2
1	MVRPLNPRPLPPVVVLMLLLLLPPSPLPLAAGDPLPTESR	1 MFLAT--LYFAIL--PLLDLSSA--EVSGGD--RL--DCVKA	1 MILANVFCCLFFFLEDTLRSLASPS--SLOQGPELHGWRPPV--DCVRANE
51	CQADPTCSAAAYHHLDSCTSSISTPLP-SEEPSVPADCLEAA	51 CQADPTCSAAAYHHLDSCTSSISTPLP-SEEPSVPADCLEAA	51 CQADPTCSAAAYHHLDSCTSSISTPLP-SEEPSVPADCLEAA
36	CLKEQS C STKYRTL RQC VAGKETNFSLASGLEAKDEC	36 CLKEQS C STKYRTL RQC VAGKETNFSLASGLEAKDEC	36 CLKEQS C STKYRTL RQC VAGKETNFSLASGLEAKDEC
47	CAAESNCSSR YRTL RQC LAGRDRN-----TMLANKE	47 CAAESNCSSR YRTL RQC LAGRDRN-----TMLANKE	47 CAAESNCSSR YRTL RQC LAGRDRN-----TMLANKE
100	GCMCHRRMKNQVACLDIYWTVH RARSLGNYEVDSPYE	100 GCMCHRRMKNQVACLDIYWTVH RARSLGNYEVDSPYE	100 GCMCHRRMKNQVACLDIYWTVH RARSLGNYEVDSPYE
86	NCRCKRGMKKEKNCLR IYWSM YQSL-QGNDLLED	86 NCRCKRGMKKEKNCLR IYWSM YQSL-QGNDLLED	86 NCRCKRGMKKEKNCLR IYWSM YQSL-QGNDLLED
92	DCRCKRGMKKELQCLQIYWSIHLGLTEGEEFYEA	92 DCRCKRGMKKELQCLQIYWSIHLGLTEGEEFYEA	92 DCRCKRGMKKELQCLQIYWSIHLGLTEGEEFYEA
150	SKL-----NMLKPDSDLCLKFAMLCTLN	150 SKL-----NMLKPDSDLCLKFAMLCTLN	150 SKL-----NMLKPDSDLCLKFAMLCTLN
135	VPFIS--VEHI--PKGNNCLDAAKACNLDD	135 VPFIS--VEHI--PKGNNCLDAAKACNLDD	135 VPFIS--VEHI--PKGNNCLDAAKACNLDD
142	ASIFSGTGADPVVS AKS NH	142 ASIFSGTGADPVVS AKS NH	142 ASIFSGTGADPVVS AKS NH
188	GPHCQRHVCLRQLLTFFEKAAEPHAQGLL	188 GPHCQRHVCLRQLLTFFEKAAEPHAQGLL	188 GPHCQRHVCLRQLLTFFEKAAEPHAQGLL
179	NDVCNRRKCHKALRQFFDKVP	179 NDVCNRRKCHKALRQFFDKVP	179 NDVCNRRKCHKALRQFFDKVP
192	PAKHSYGM	192 PAKHSYGM	192 PAKHSYGM
238	LCPCAPNDRGCGERRRNTIAPP	238 LCPCAPNDRGCGERRRNTIAPP	238 LCPCAPNDRGCGERRRNTIAPP
227	LCRSLIVDFQTHCHP-MDILGTCATEQ	227 LCRSLIVDFQTHCHP-MDILGTCATEQ	227 LCRSLIVDFQTHCHP-MDILGTCATEQ
240	LCRSLADFFTNCOPESRSVSSCLKEN	240 LCRSLADFFTNCOPESRSVSSCLKEN	240 LCRSLADFFTNCOPESRSVSSCLKEN
286	QSRCLRAYLGLIGTAMTPNFVSNV--NTSVALSCT	286 QSRCLRAYLGLIGTAMTPNFVSNV--NTSVALSCT	286 QSRCLRAYLGLIGTAMTPNFVSNV--NTSVALSCT
277	TCRGSGNLQEECEMLE	277 TCRGSGNLQEECEMLE	277 TCRGSGNLQEECEMLE
290	TCRGSGNLQEECEMLE	290 TCRGSGNLQEECEMLE	290 TCRGSGNLQEECEMLE
333	YADCLLAYSGLIGTVMTPNYIDSS--SLSVAPWCD	333 YADCLLAYSGLIGTVMTPNYIDSS--SLSVAPWCD	333 YADCLLAYSGLIGTVMTPNYIDSS--SLSVAPWCD
325	CSNSGNLQEECEMLE	325 CSNSGNLQEECEMLE	325 CSNSGNLQEECEMLE
340	CRGSGNMEEECEKFL	340 CRGSGNMEEECEKFL	340 CRGSGNMEEECEKFL
358	YQACLGSYAGMIGFD	358 YQACLGSYAGMIGFD	358 YQACLGSYAGMIGFD
375	DMTPNYVDSSPTGIVVSPWCS	375 DMTPNYVDSSPTGIVVSPWCS	375 DMTPNYVDSSPTGIVVSPWCS
390	CRGSGNMEEECEKFL	390 CRGSGNMEEECEKFL	390 CRGSGNMEEECEKFL
381	QDWPHPTFAVMAHQNENPAVRPQ--	381 QDWPHPTFAVMAHQNENPAVRPQ--	381 QDWPHPTFAVMAHQNENPAVRPQ--
425	PAGSENEIPTHVLPPPCANLQAOQKLLKSNVSGNTHL	425 PAGSENEIPTHVLPPPCANLQAOQKLLKSNVSGNTHL	425 PAGSENEIPTHVLPPPCANLQAOQKLLKSNVSGNTHL
435	CISNGNYEKEGLGAS	435 CISNGNYEKEGLGAS	435 CISNGNYEKEGLGAS
450	DLTQAPRVEKTPSLPDDLS	450 DLTQAPRVEKTPSLPDDLS	450 DLTQAPRVEKTPSLPDDLS
481	PTWVPSLFSCTLPLILLLSLW--	481 PTWVPSLFSCTLPLILLLSLW--	481 PTWVPSLFSCTLPLILLLSLW--
525	HITTKSMAAPPSCGLSP	525 HITTKSMAAPPSCGLSP	525 HITTKSMAAPPSCGLSP
545	LLVTVVTA	545 LLVTVVTA	545 LLVTVVTA
565	STL	565 STL	565 STL
585	LSLT	585 LSL	585 LSL
605	ETS	605 ETS	605 ETS
625	KVIKPN	625 KVIKPN	625 KVIKPN
645	SGPSRA	645 SGPSRA	645 SGPSRA
665	RPSSA	665 RPSSA	665 RPSSA
685	LT	685 LT	685 LT
705	VLSV	705 VLSV	705 VLSV
725	MLKQAL	725 MLKQAL	725 MLKQAL

FIG. 6

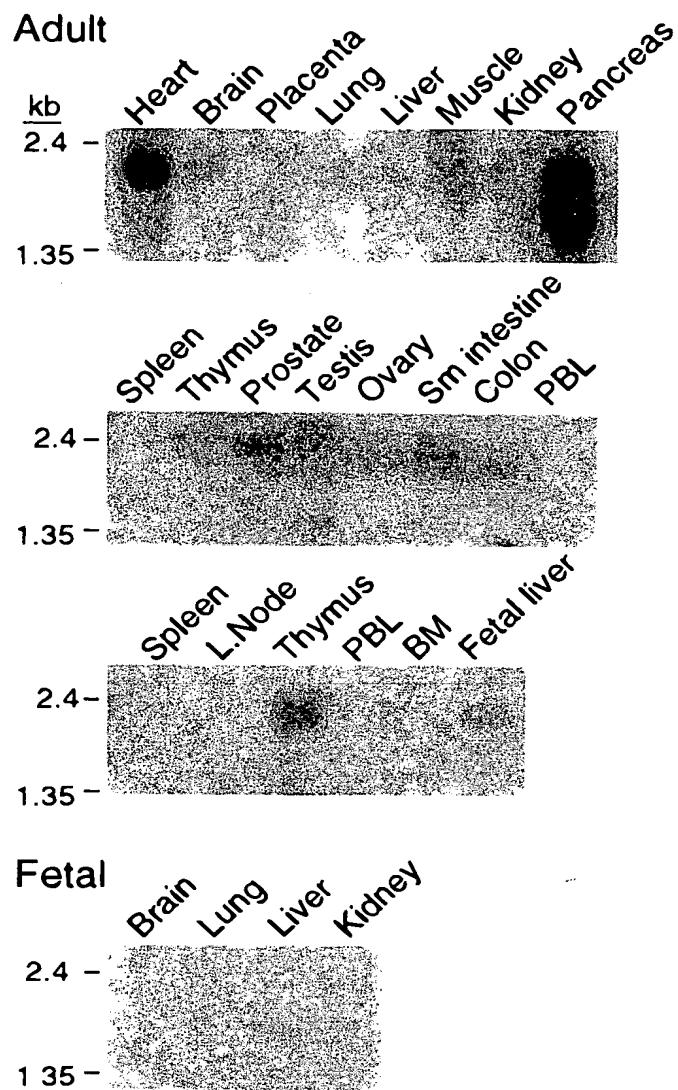


FIG. 7

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$GFR\alpha 1$

$GFR\alpha 2$

$GFR\alpha 3$

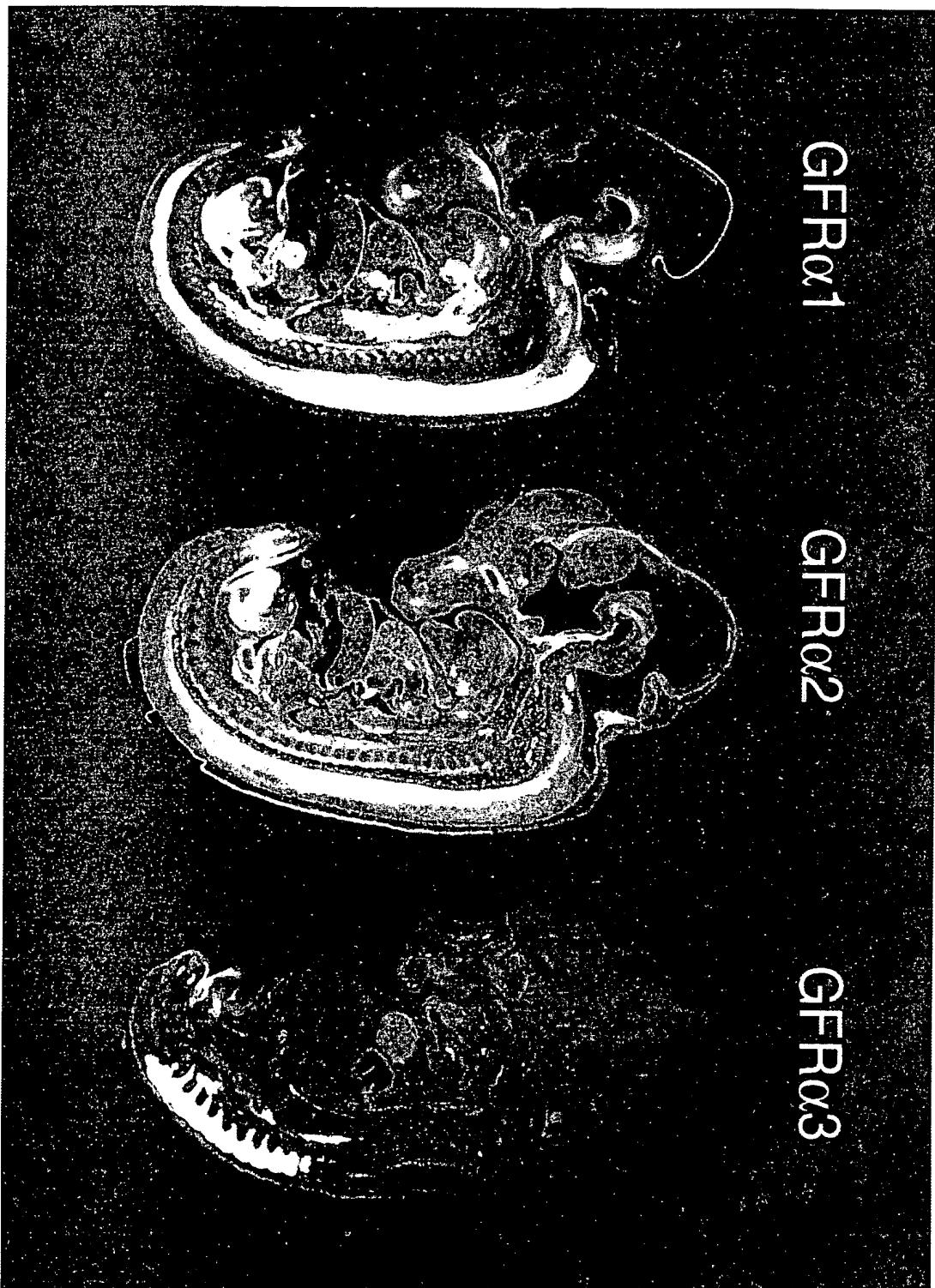
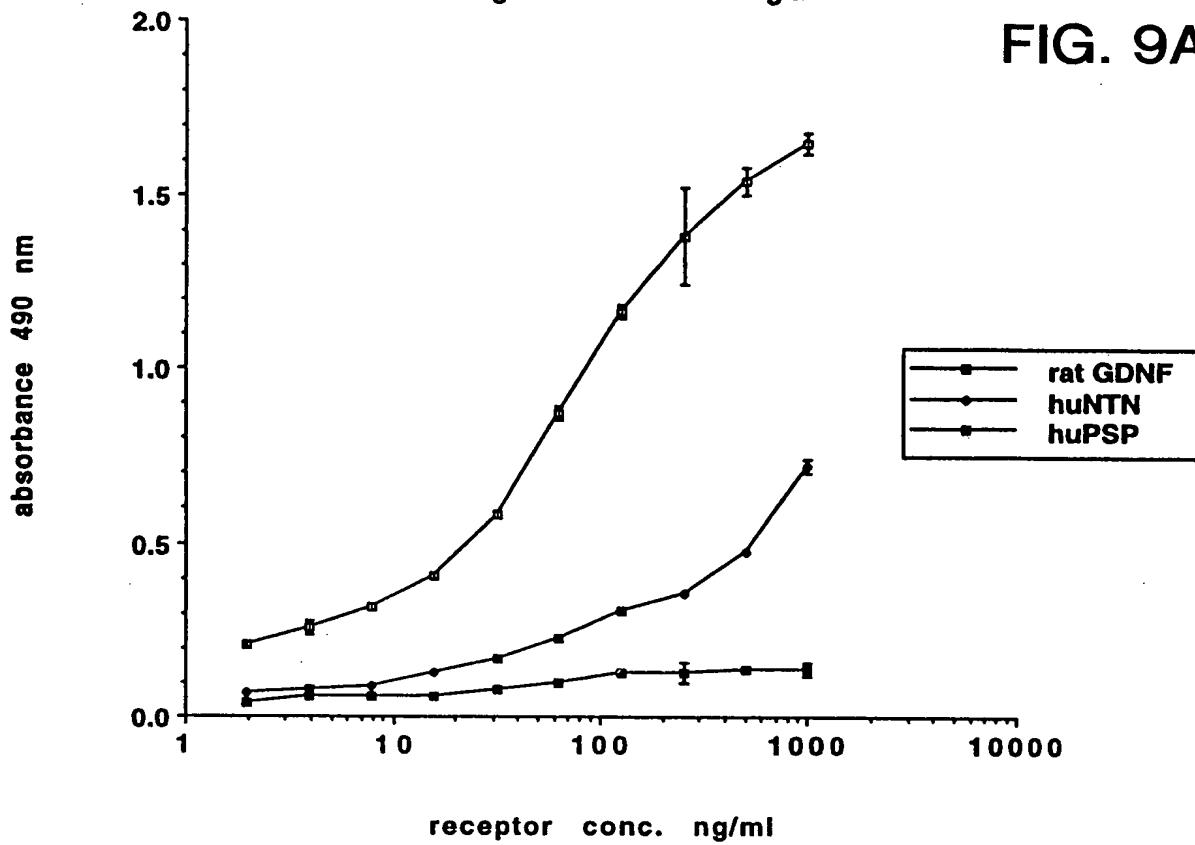
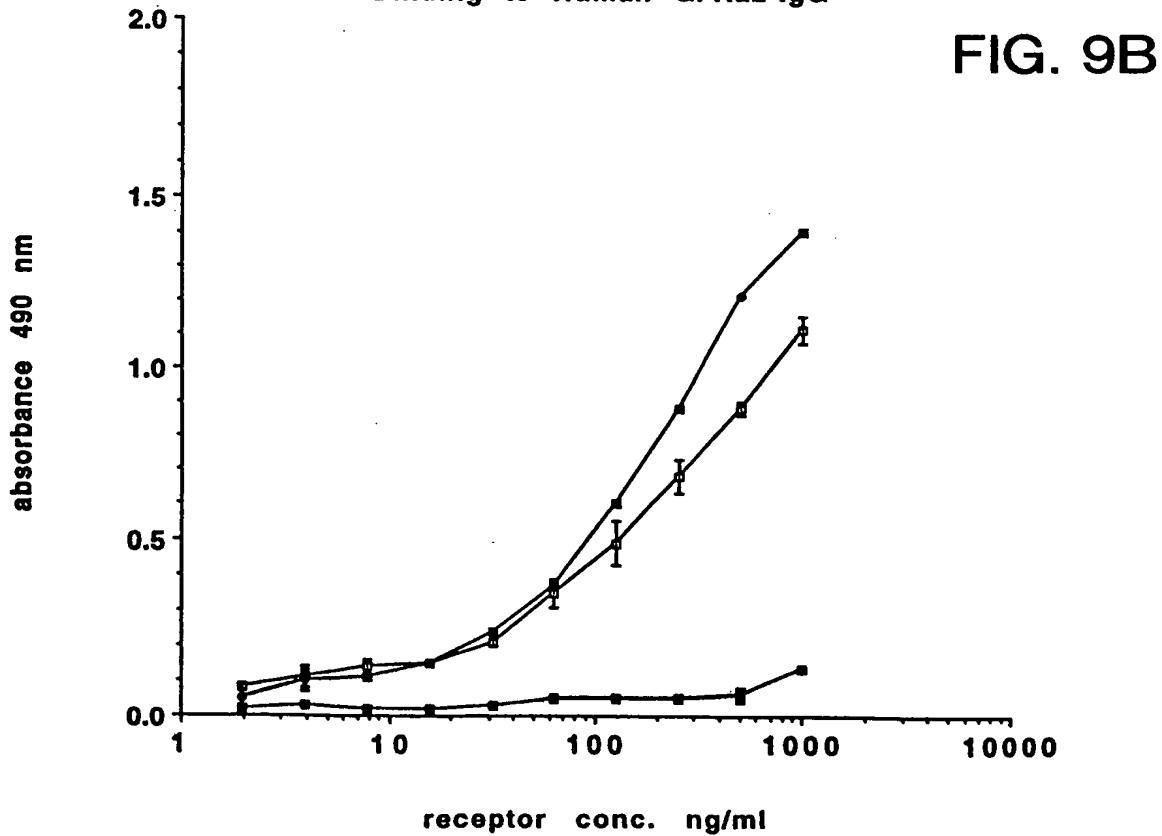


FIG. 8

Binding to Rat GFR α 1-IgG



Binding to Human GFR α 2-IgG



Binding to Human GFR α 3-IgG

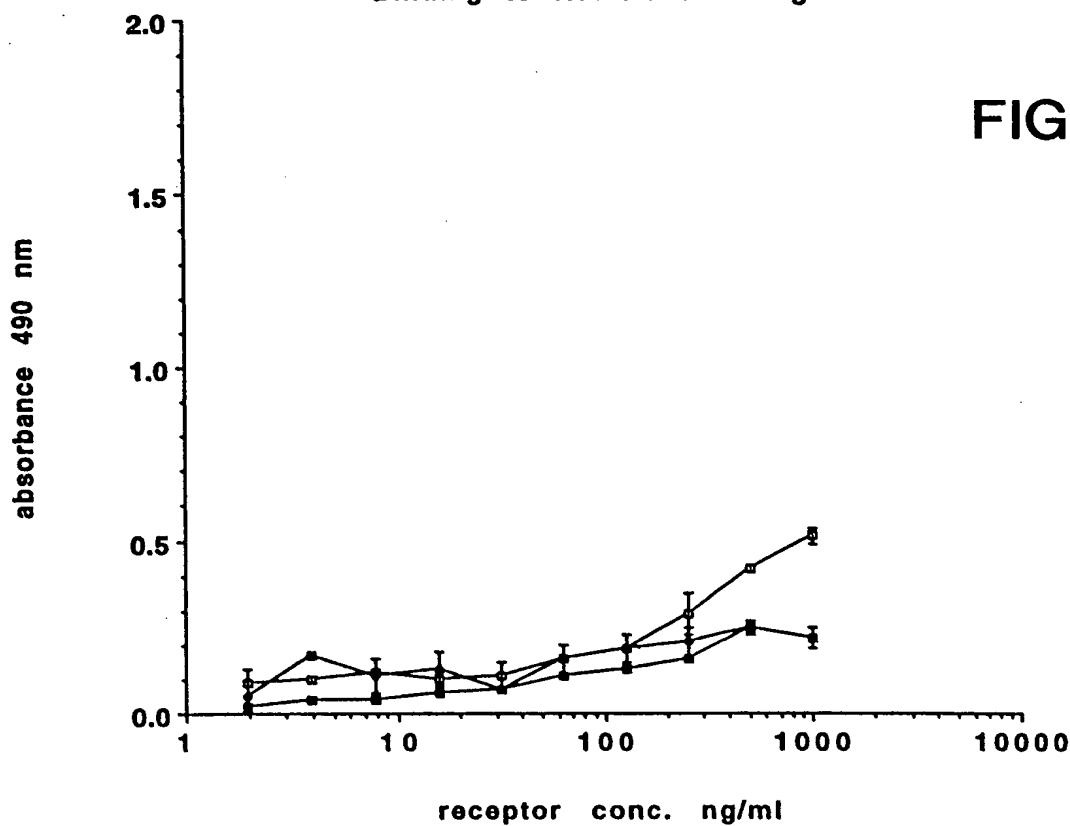


FIG. 9C

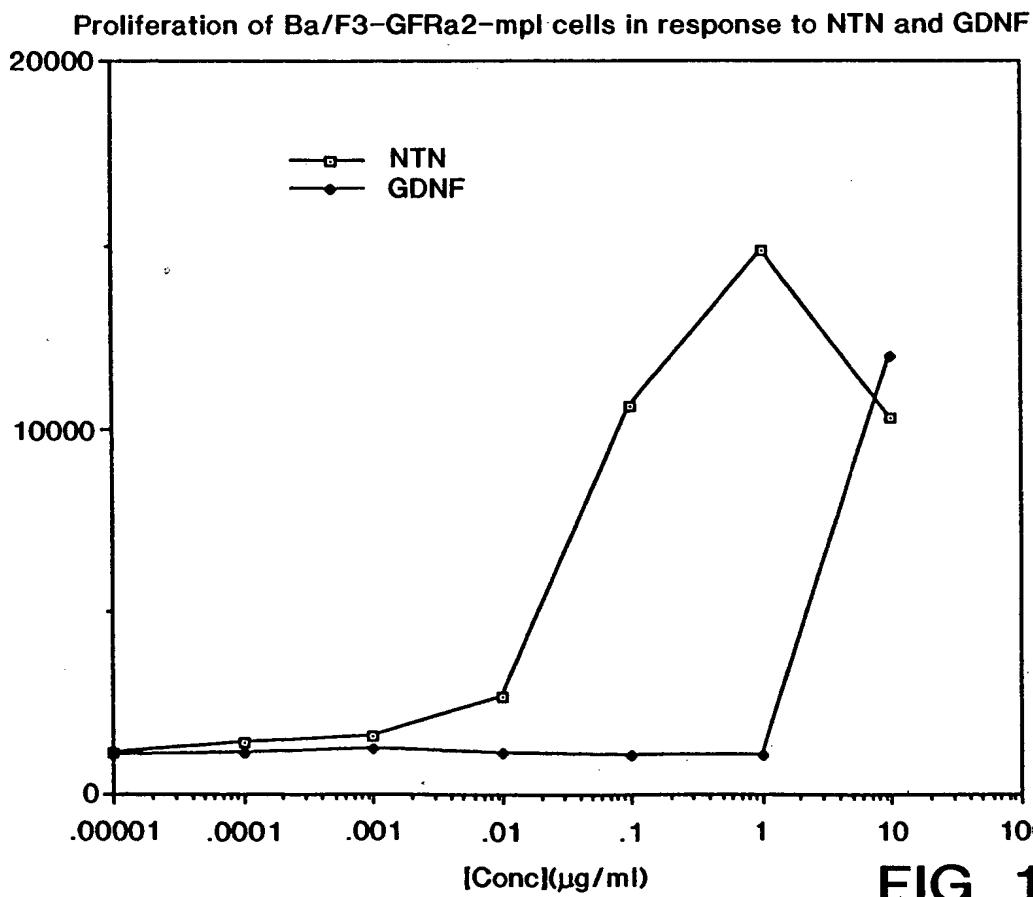


FIG. 10

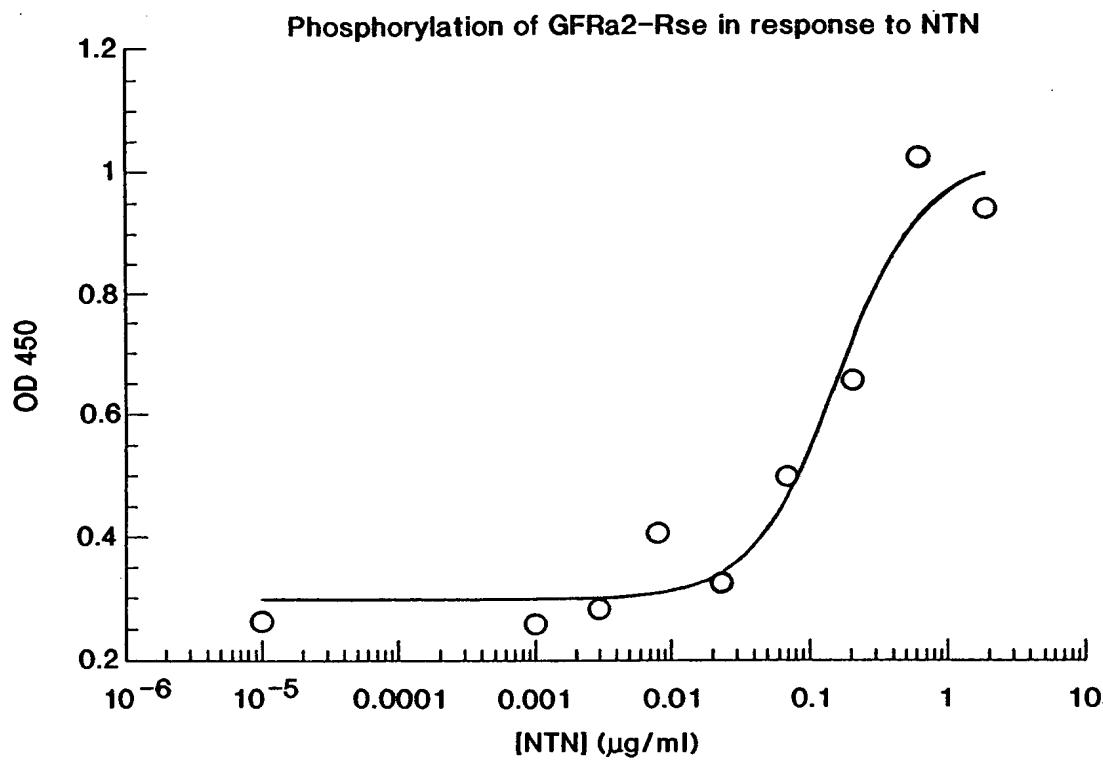


FIG. 11

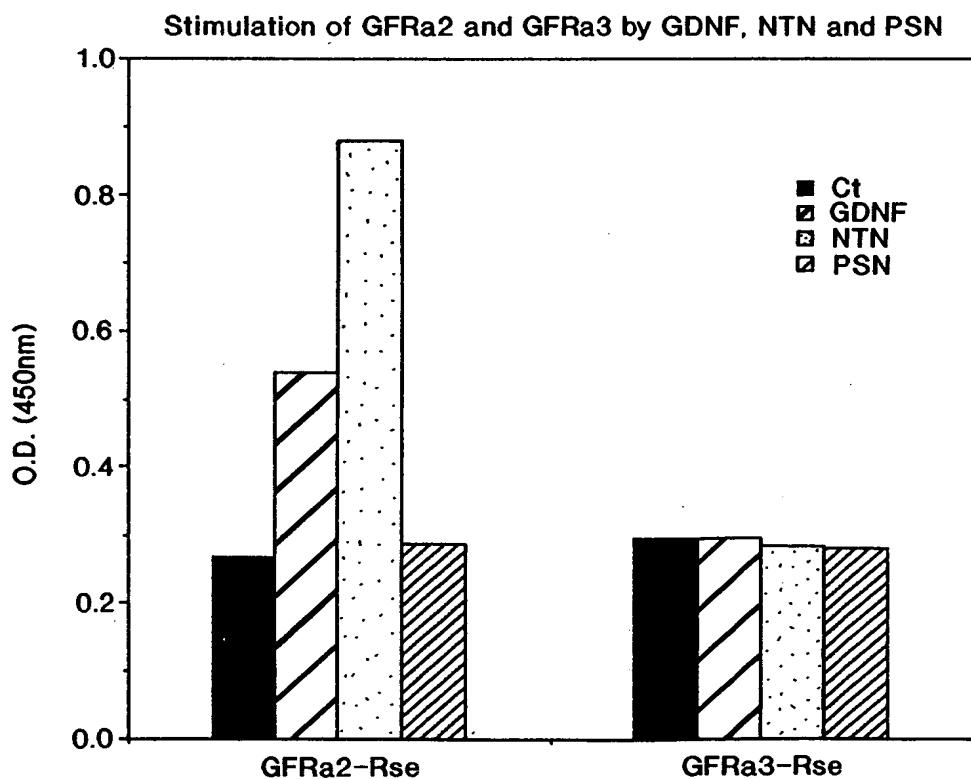


FIG. 12

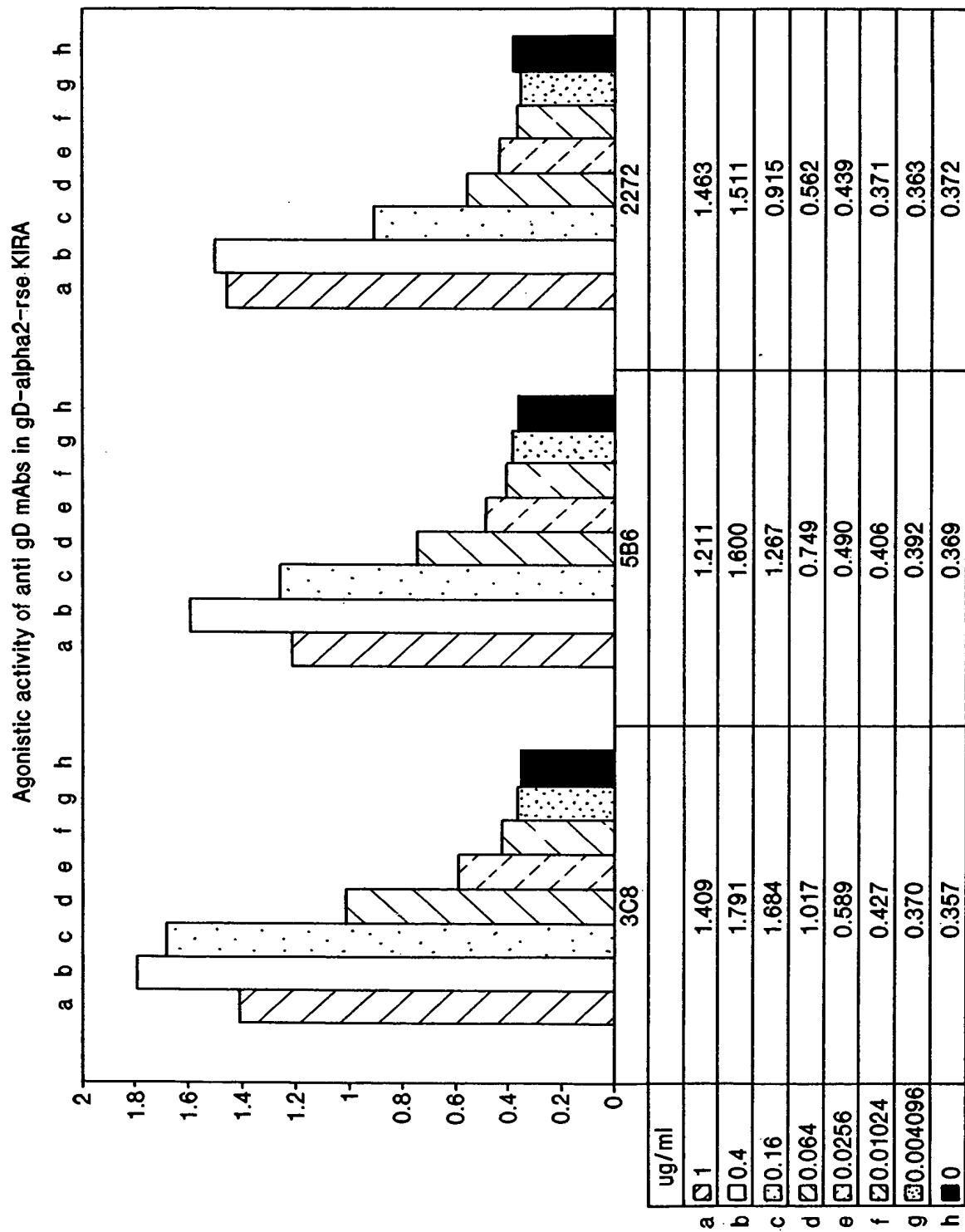


FIG. 13